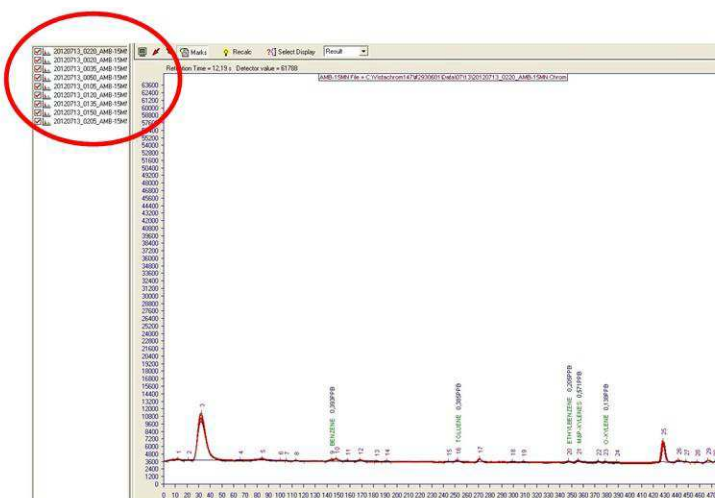


## HOW TO PERFORM A "POST-PROCESS"

- Open the Peak Viewer.
- Select the Chromatograms you want to "post-process":

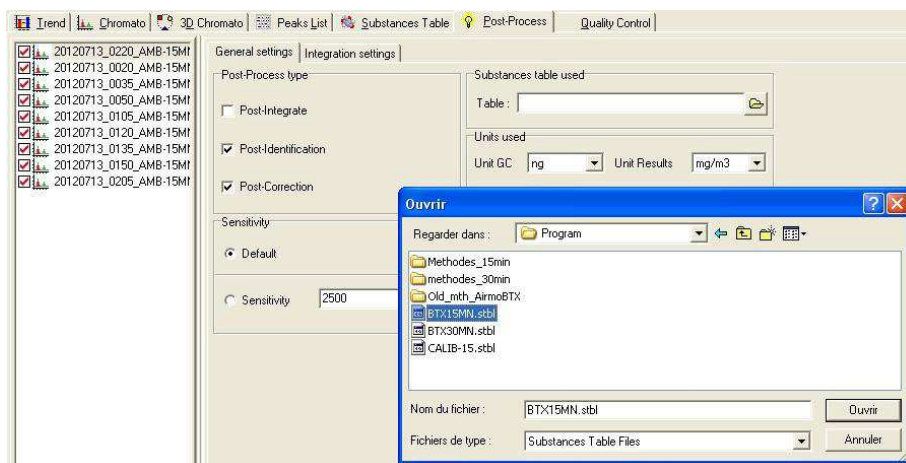


- On the "Post-Process" tab:

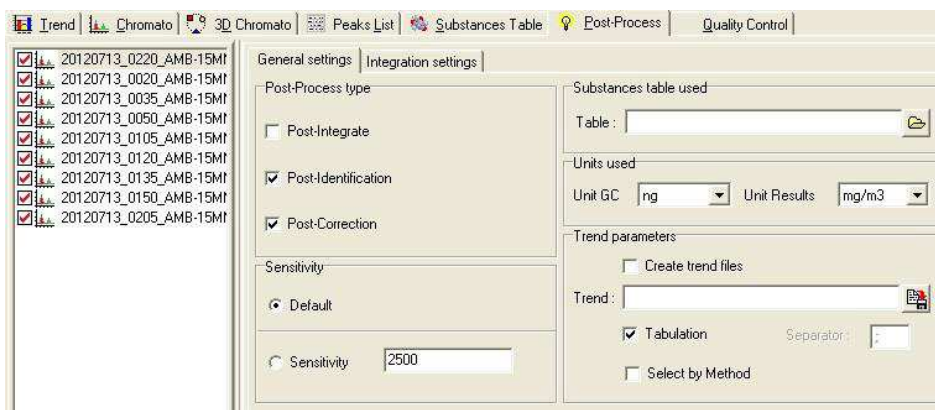
Choose the post-process type you want to apply to the chromatograms you have selected.

- Post-Integrate: you want to do a new integration of the peaks (you will have to use the "Integration setting" tab, when you select this option).
  - Post-Identification: you want to do a new identification of the peaks: a new name appears on the peak which is now correctly integrated.
  - Post-Correction: you want to calculate the concentration of the compounds (using a new sensitivity or a new response factor ...).
- Choose the Base Sensitivity (BS) you want to use to do the concentration calculations of the compounds:
    - "Default": the sensitivity of the analyzer will be used.
    - You can also write the sensitivity you want to use, by choosing the second option.

- Choose the Unit you want to use for concentration results of the compounds:
  - “Unit GC”: corresponds to Factory unit:
    - ng: for analyzer with a trap (airmoVOC, airTOXIC, airmoBTX...)
    - mg/m3: for analyzer with a loop (chromaTHC, chromaFID, chroma PID, chroma S, MEDOR...)
  - “Unit Results”: corresponds to the unit you want.
- Then select the substance table you want to apply to the chromatograms:



- If you want to create new ASCII files (you can open with Excel) during the post-process, select the option: “Create Trend files”.



(You need to open these ASCII files on another computer, because there is not Excel software on the integrated PC.)

- Then, to start the post-process, click on:



- To see the results (after the “post-process”) appearing on the screen, return to the “Chromato” tab, and click on:



**Remark:** You can choose to see the post-processed results appearing on the Chromatogram, selecting this option. If you want to return to the original data, unselect “Recalc”.